



PATENT
2798-1-001

**IN THE UNITED STATES PATENT AND TRADEMARK
OFFICE**

Applicant: Alfonso Fernández-Mayoralas Alvarez Examiner : Underdahl, Thane E.

Serial No.: 10/738,378 Group Unit : 1651

Filed: December 17, 2003

For: ENZYMATIC METHOD OF PRODUCING 4-O- β -D-GALACTOPYRANOSYL-D-XYLOSE, 4-O- β -D-GALACTOPYRANOSYL-D-XYLOSE OBTAINED USING SAID METHOD, COMPOSITIONS CONTAINING SAME AND THE USE THEREOF IN EVALUATING INTESTINAL LACTASE

DECLARATION UNDER 37 C.F.R. 1.132

COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

I, Alfonso Fernández-Mayoralas Alvarez, as evidenced by my signature below, declare the following:

1. I received a Ph.D. in Chemistry in 1987 from Autónoma University of Madrid (Spain). I received a Master's Degree in Chemistry in 1983 from Autónoma University of Madrid. I received a Bachelor's Degree in Chemistry in 1982 from Autónoma University of Madrid.

2. In addition to the academic appointments set forth in paragraph 1, *supra*, I was a Research Scientist at various public institutions (see Exhibit A) from 1985 - 2007.

3. My research interests include developing synthesis processes for 4-galactosyl-xylose. A detailed chronology of my academic and professional accomplishments is submitted herewith in my *Curriculum Vitae*, Exhibit A.

4. I have reviewed the above-referenced United States patent application, Serial Number 10/738,378, the subject matter described therein as well as the currently pending claims in the application and Reyes *et al.*, U.S. Patent 5,994,092, Ponpipom *et al.*, U.S. Patent 4,228,274, Crumpton *et al.*, *Biochem. J.* 70(4):729 (1958), Wong-Madden *et al.*, U.S. Patent 5,770,405, Dahmen *et al.*, U.S. Patent 4,675,392, Rao *et al.*, *Qual. Plant.-Pl. Fds. Hum. Nutr. XXVIII* 4:293-303 (1979), Gabelsberger *et al.*, *FEMS Letters* 109(2-3): 131 (1993), Fujimoto *et al.*, *Glycoconjugate Journal* 15:155 (1998) and Yoshitake *et al.*, *Eur. J. Biochem.* 101:395 (1979).

5. The claims pending in the above-referenced patent application are directed to obtaining a product useful for evaluating intestinal lactase. In the process described two parts can be distinguished, namely an enzyme reaction and a subsequent purification of the reaction mixture. Developing a method for purifying a carbohydrate mixture is neither easy nor routine for one skilled in the art, due at least in part to the characteristics of carbohydrate molecules.

6. The chemistry of carbohydrates is very complex, since different carbohydrate molecules have very similar structures. Many carbohydrates even have the same molecular formula. For example, lactose and sucrose both have 12 carbons, 22 hydrogens and 11 oxygens and the same type of functional group (the hydroxyl group).

7. Small changes in the structure of carbohydrates (for example, two carbohydrates that differ in the stereochemistry of one of their chiral centres, such as cellobiose and lactose, can give rise to significant differences both in chemical reactivity and in behavior in the purification processes. Raymond Lemieux opined the following: "*The only generalization that*

exists in the chemistry of carbohydrates is that there is no generalization. "

8. Applicants submit herewith two additional journal articles that each further describe some of the complexities and problems associated with carbohydrate chemistry, Marcaurelle *et al.*, *Current Opinion in Chemical Biology*, 2002, 6:289-296 (Exhibit B) and Holemann *et al.*, *Current Opinion in Biotechnology*, 2004, 15:615-622 (Exhibit C).

9. Although crystalization is in fact a common process for purifying sugars, finding the appropriate solvent is not easy. The appropriate solvent depends on the type of molecules and the range of solvents that must be tested can be very broad. The more customary solvents in sugars tend to be low molecular weight alcohols, water, ethyl acetate, hexane, and their mixtures. In a crystallization process, a large number of solvents and mixtures thereof must be tested or screened before arriving at the appropriate solvent to use. In the case of the above-referenced patent application, acetone allows obtaining the product desired with a >99% degree of purity, which was not possible with more usual solvents. In Exhibit D a gas chromatogram of the 4-galactosyl-xylose obtained by the process described in the above-referenced patent application, can be shown. Peaks at retention times of 18.70 and 18.92 min correspond to alpha and beta anomers of 4-galactosyl-xylose, respectively. By simply summing the % areas of each peak ($92,566 + 6,540 = 99,106\%$), a purity of over 99% is achieved.

10. Wong-Madden *et al.*, U.S. Patent 5,770,405 do not use the solvent mixture in a chromatography on active carbon. Wong-Madden *et al.* teach using isopropanol/ethanol/water, but it is to develop a chromatography on silica gel. (See, Column 33, line 25).

11. Active carbon is customarily used to eliminate hydrophobic impurities, but it is not normally used in organic synthesis, for separating monosaccharide and disaccharide mixtures, such as is the case in the above-referenced patent application. The normal course to separate these mixtures is to employ chromatography on a silica gel, on sepharose or others (See, Wong-Madden *et al.*, Column 11, line 19). The above-referenced patent application

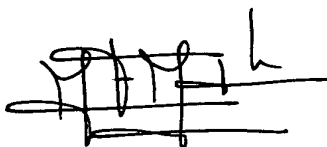
describes purifying a mono- and disaccharide mixture using active carbon, which offers the advantage, compared with usual adsorbents (e.g., silica gel or sepharose) of being cheaper. In H. Rotzche, *Journal of Chromatography Library* 1991, 48:104-107 (Exhibit E), either structural and geometrical differences between each kind of adsorption matrixes, active carbon in comparison with other column fillings as polymers, silica gel, etc. are discussed in detail.

12. The above-referenced patent application describes an isopropanol/water mixture as eluent, as opposed to the more common alcohol/water mixtures such as methanol/water or ethanol/water. The methods described in the above-referenced patent application thereby provide the advantage of allowing for less elution volume, a significant advantage for industrial production (Exhibit F).

13. Rao *et al.* teach extraction with Soxhlet to extract fats from a specimen of plant origin. Rao *et al.* do not describe using Soxhlet for selectively extracting monosaccharides from a mixture of sugars.

14. All statements made herein of my own knowledge are true and all statements made on information and belief are believed to be true; and further these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code; and that such willful false statements may jeopardize the validity of the application, or any patent issuing thereon.

Submitted by



Alfonso Fernández-Mayoralas Alvarez

Date Signed: May 31, 2007

CURRICULUM VITAE

Name: Alfonso Fernández-Mayoralas Alvarez

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1. ACADEMIC DEGREES

- Degree In Chemistry (BSC). Autónoma University of Madrid (Spain). 1982.
- Ph. D. In Chemistry. Autónoma University of Madrid. 1987. *Cum Laude*

2. PROFESSIONAL EMPLOYMENTS AND RESEARCH EXPERIENCE

- **1985-1987.** Graduent Student. Fellow of the MEC. Organic Chemistry Institute. CSIC. Supervisor: Dr. Manuel Martín-Lomas.
- **1988.** Postdoctoral Fellow, École Normale Supérieure, Paris. Supervisor: Dr. Pierre Sinaÿ
- **1989.** Posdoctoral Fellow. Massachusetts Institute of Technology. Supervisor: Dr. A.M. Klibanov
- **1990-2002.** Tenure Scientist at the Department of Biological Chemistry, Institute of Organic Chemistry, C.S.I.C. Madrid (Spain).
- **1991 (4 months).** Visiting Scientist at the Chemical Center, Lund (Sweden). Supervisor: Dr. K. G. I. Nilsson.
- **2002-.** Scientific Researcher at the Department of Biological Chemistry, Institute of Organic Chemistry, C.S.I.C. Madrid (Spain).

3. MAIN RESEARCH INTEREST

Carbohydrate chemistry. Synthesis of glycoconjugates with biological significance. Use of enzymes in organic synthesis.

4. PUBLICATIONS

A. Fernández-Mayoralas y M. Martín-Loma. Synthesis of 3-O-methyl and 4-O-methyltetra-O-acetyl- α -D-galactopyranose. *Anal. Quim.*, 80C (1984) 184-185.

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4. PATENTS

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Combinatorial carbohydrate chemistry

Lisa A Marcaurelle and Peter H Seeberger*

The application of combinatorial chemistry to the synthesis of carbohydrate-based compound collections has received increased attention in recent years. New strategies for the solution-phase synthesis of oligosaccharide libraries have been reported, and the use of monosaccharides as scaffolds in the generation of combinatorial libraries has been described. Novel approaches to the assembly of carbohydrate-based antibiotics, such as aminoglycoside analogs and vancomycin derivatives, have also been disclosed.

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Abbreviation

RGD Arg–Gly–Asp

Introduction

Combinatorial chemistry has become an important tool in modern drug development. Although carbohydrate-based compounds hold great potential as therapeutic agents, the application of combinatorial chemistry to this class of biomolecules has only recently elicited attention. The challenges associated with carbohydrate synthesis, including laborious protecting group manipulations and the need for regioselective and stereoselective glycosylation reactions, are primarily responsible for the lack of more intense efforts. The high degree of functionalization and diverse stereochemistry of carbohydrates, the very properties that render them attractive members of compound libraries, are responsible for the complications encountered by the experimentalist. In addressing and overcoming these challenges, the synthesis of a number of carbohydrate-based libraries has been achieved. This review highlights recent progress in the combinatorial synthesis of carbohydrates, including the development of new carbohydrate-based antibiotics and the use of carbohydrates as scaffolds for the synthesis of stereodiverse libraries. Recent advancements in solid-phase oligosaccharide synthesis and its application to carbohydrate libraries is also discussed.

Several excellent articles reviewing combinatorial carbohydrate synthesis have appeared prior to 2000 [1*,2,3]. This article focuses primarily on strategies reported in the past two years. The synthesis of glycopeptide libraries and related glycoconjugates has been reviewed recently and thus will not be covered [4**,5].

Combinatorial oligosaccharide libraries

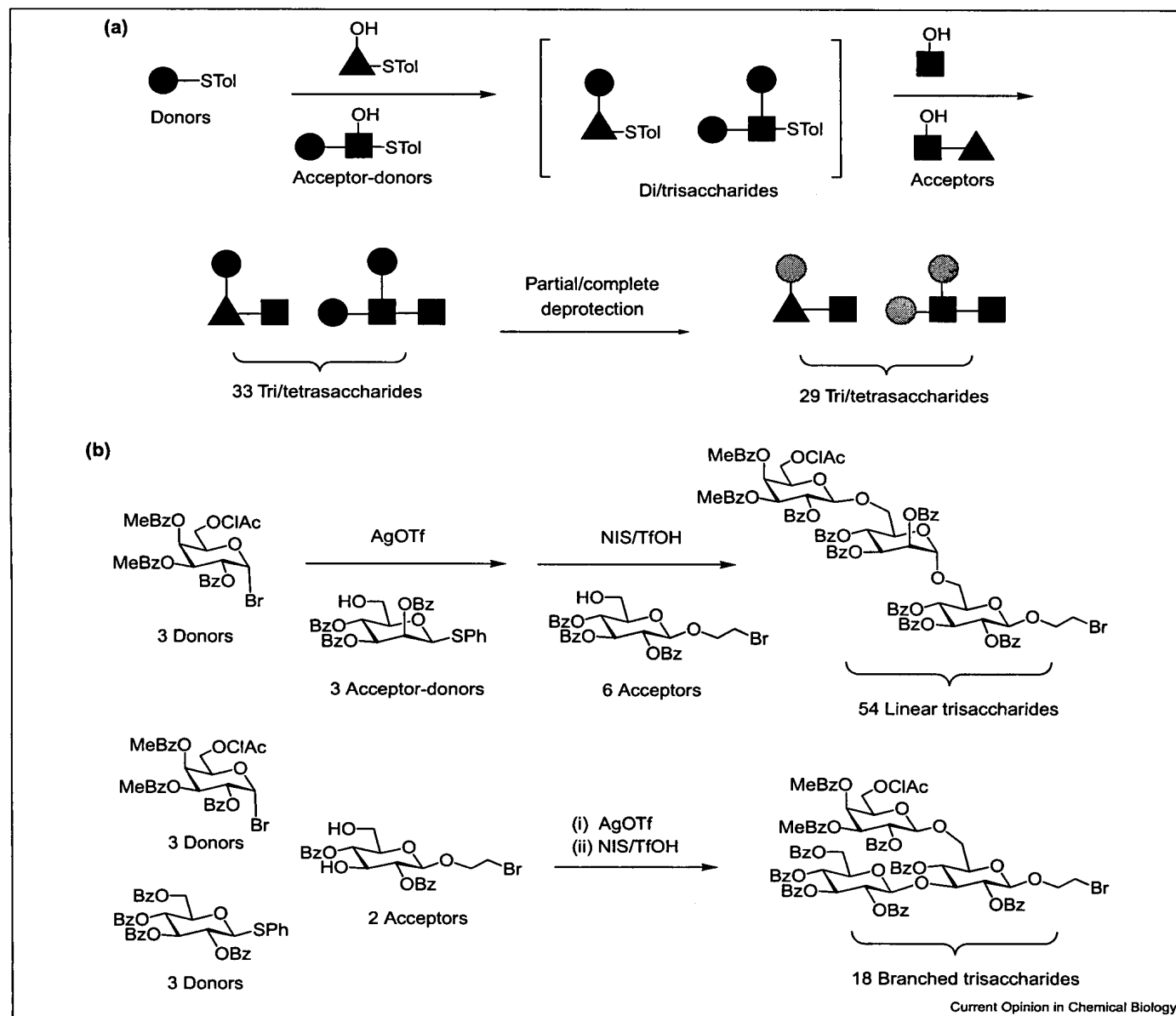
In the past five years, the combinatorial synthesis of oligosaccharide libraries has been carried out both in

solution and on solid support [1*,2,3]. During the period covered by this review, only two approaches to the combinatorial synthesis of oligosaccharides have been reported [6**,7*]. Both reports describe similar solution-phase approaches, employing sequential one-pot glycosylation strategies. Ye and Wong [6**] made use of their programmable one-pot glycosylation technology [8], which has been employed for the synthesis of a number of structures, including the tumor-associated hexasaccharide Globo-H [9*]. With the aid of anomeric reactivity values determined with the computer program OptiMer™, the construction of a small library of trisaccharides and tetrasaccharides was accomplished using a panel of monosaccharide and disaccharide donors. The sequential reaction of thioglycosides of varying reactivity produced a library of 33 oligosaccharides, which were partially or completely deprotected to create 29 additional compounds (Figure 1a).

In the second approach, Takahashi *et al.* [7*] reported the rapid assembly of a library of linear and branched trisaccharides by using a combination of donors, including glycosyl bromides, thioglycosides and 2-bromoethyl glycosides (Figure 1b). Selective activation of the bromide and thioglycoside donors with AgOTf and NIS/TfOH, respectively, enabled the generation of a library of 72 trisaccharides by sequential one-pot reactions on a manual synthesizer. It should be noted that each member of the library contains two sites for further elaboration. The chloroacetate group can be selectively removed for attachment of the trisaccharide to solid-support, while the bromoethyl glycoside can be modified by alkylation for the introduction of diversity at the anomeric position.

The synthesis of oligosaccharide libraries in solution has been quite fruitful. Still, the use of solid-phase methods for the construction of glycosidic linkages is attractive, because an excess of reagents may be used to ensure high yields and the number of purification steps is reduced. The solid-phase synthesis of oligosaccharide libraries was first reported by Kahne and co-workers [10] and later by Zhu and Boons [11]. Although no new methods for the solid-phase synthesis of oligosaccharide libraries have been reported during the past two years, a number of strategies for the solid-phase synthesis of oligosaccharides in general have been reported [12–14,15**,16*], including the automation of oligosaccharide assembly. The first automated solid-phase oligosaccharide synthesizer [15**] was used to prepare structures as large as branched dodecamers in less than one day. The synthesis was achieved using a re-engineered peptide synthesizer containing a coolable reaction vessel, utilizing glycosyl phosphates and glycosyl trichloroacetimidate building blocks (Figure 2). Each cycle involved the coupling of a building block to a growing resin-bound oligosaccharide and the removal of a protecting group to expose a single hydroxyl

Figure 1



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Novel approaches to oligosaccharide libraries. (a) Wong's approach to the one-pot assembly of a library of linear and branched trisaccharides and tetrasaccharides. The sequential reaction of thioglycoside donors of varying reactivity produced a library of 33 oligosaccharides, which were partially or completely deprotected to afford 29 more compounds.

(b) Takahashi's one-pot sequential assembly of a library of trisaccharides. Selective activation of glycosyl bromide and thioglycoside donors with AgOTf and NIS/TfOH, respectively, yielded a library of 72 linear and branched trisaccharides. Bz, benzoyl group; NIS, *N*-iodosuccinimide; TfOH, trifluoromethanesulfonic acid.

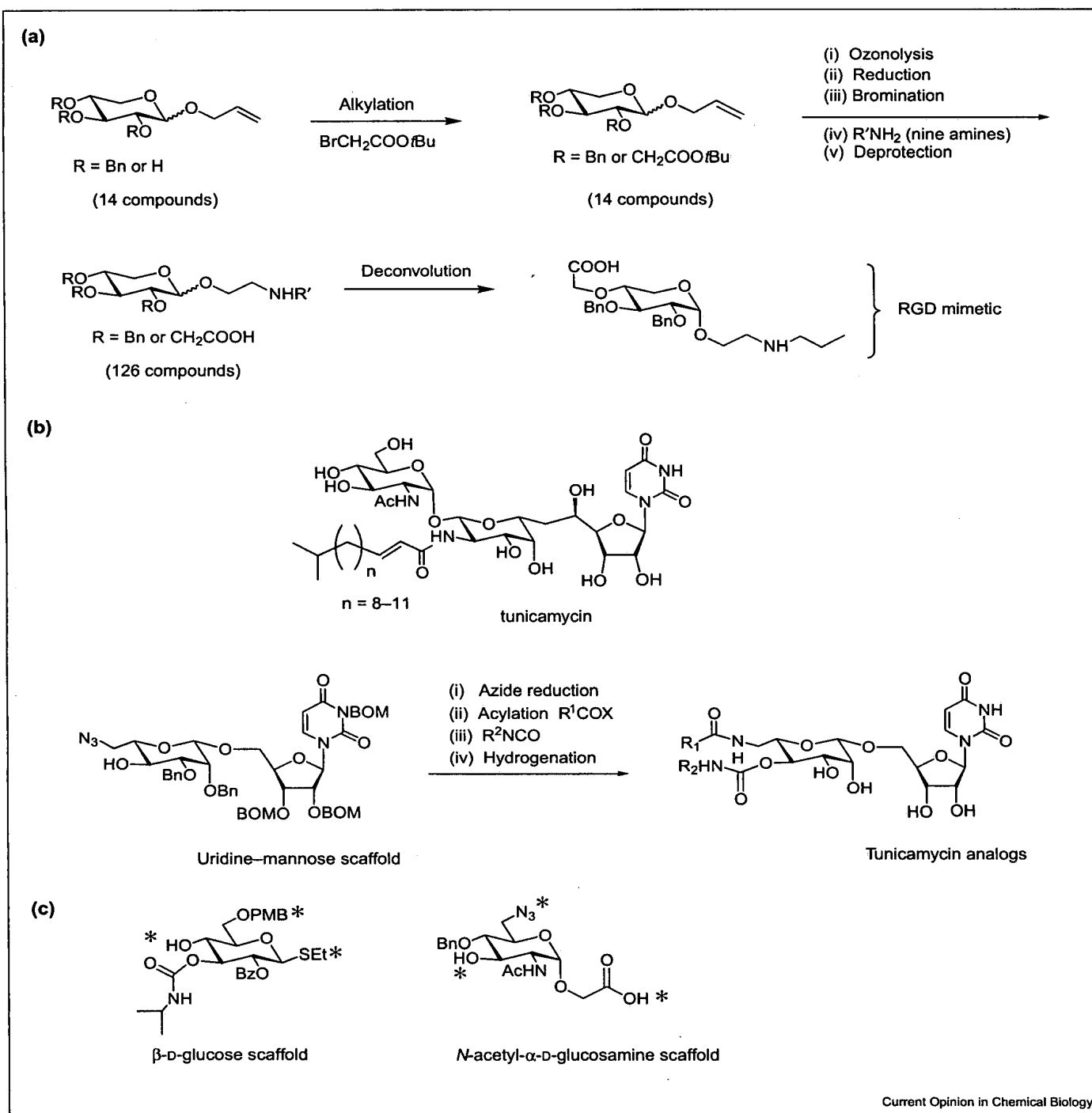
group for attachment of the next carbohydrate. A meta-thesis-cleavable octenediol linker enabled release of the oligosaccharide from the support using Grubb's catalyst. This method has recently been applied to the synthesis of a branched tetrasaccharide (Figure 2) corresponding to a portion of the cell-surface lipophosphoglycan of *Leishmania* parasites [16*]. Branching of the tetrasaccharide was achieved through the selective removal of different ester protecting groups. The automation of oligosaccharide synthesis

is expected to greatly facilitate preparation of oligosaccharide libraries by parallel synthesis.

Carbohydrate scaffolds for combinatorial synthesis

Monosaccharides are particularly attractive scaffolds for the synthesis of combinatorial libraries. They are readily available, conformationally rigid, chiral and highly functionalized molecules, containing up to five hydroxyl

Figure 3



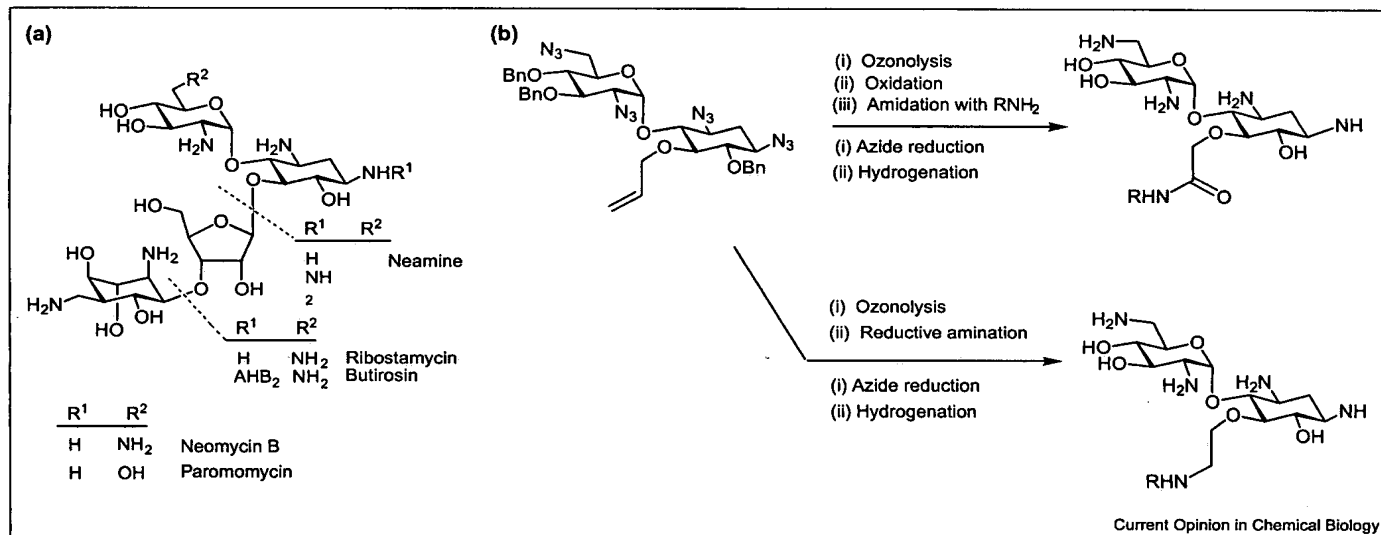
Use of carbohydrates as scaffolds for combinatorial synthesis. **(a)** Synthesis of a combinatorial library of peptidomimetics of the RGD sequence using D-xylose as a sugar scaffold [21*]. An RGD-mimic that was identified from the library is shown. **(b)** Structure of Sofia's carbohydrate scaffold based on

tunicamycin containing two sites for functionalization. [22]. **(c)** Structure of carbohydrate scaffolds derived from β -D-glucose [23] and *N*-acetyl- α -D-glucosamine [24]. Sites for functionalization are indicated (*). BOM, benzyloxy methyl; PMB, *para*-methoxybenzyl group.

aminoglycosides, such as neomycin, kanamycin and streptomycin, and the glycopeptides vancomycin and teicoplanin. Because of the recent emergence of a number

of drug-resistant bacterial strains, much effort has been focused on the generation of new structures with improved antibiotic activity. Wong and co-workers [26–28] have

Figure 4



Synthesis of aminoglycoside libraries based on neamine assembled by reductive amination and amidation [29].

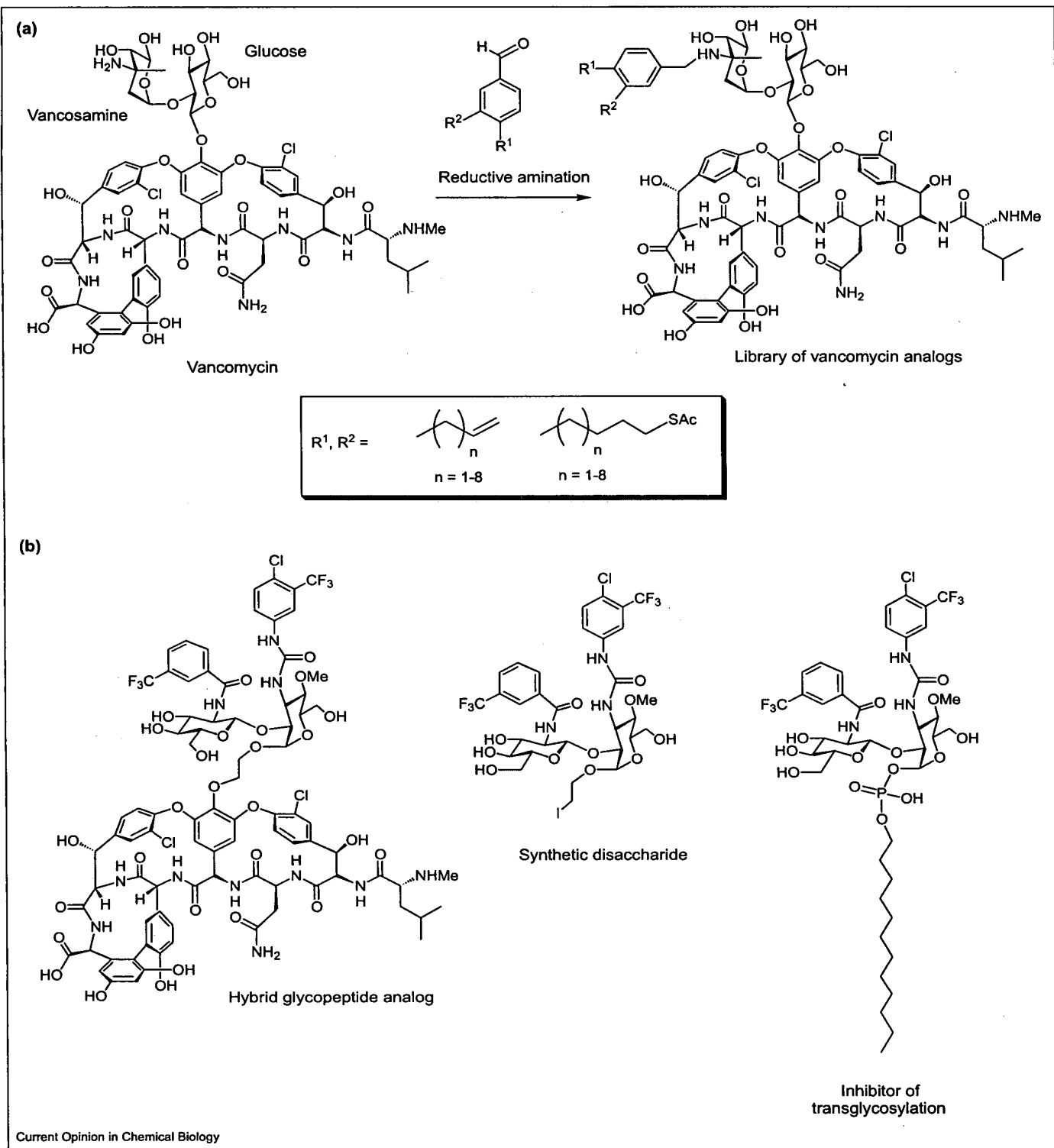
reported a number of library-based approaches for the discovery of new aminoglycoside antibiotics. Because of the size and complexity of aminoglycosides such as neomycin (Figure 4), a primary focus for the design of new antibiotics is the identification of simpler structures that retain the activity of the parent compound. Over the course of their studies, Wong *et al.* identified the naturally occurring pseudodisaccharide neamine as a core structure for the generation of new libraries of aminoglycoside mimetics [28]. A recent report described the synthesis of a library of neamine-based compounds and their RNA-binding properties [29]. The neamine library was constructed by reaction of the corresponding azide precursor with a variety of amines after conversion of the 5-*O*-allyl group to a reactive chemical handle (Figure 4). Amidation or reductive amination of the intermediate acid or aldehyde, followed by azide reduction and hydrogenation, yielded a library of compounds modified at the C-5 position of neamine.

The glycopeptide vancomycin (Figure 5a) has been used clinically for the past 40 years to treat infection by Gram-positive bacteria. The emergence of resistance to vancomycin in enterococcal strains has aroused considerable concern [30] and spurred vigorous efforts to develop novel antibiotics to combat these strains. In a series of recent reports, Nicolaou and co-workers [31,32,33**] described the construction of several libraries of vancomycin analogs, modified within the carbohydrate portion of the glycopeptide. Initial efforts were directed towards the replacement of the naturally occurring disaccharide with a panel of synthetic monosaccharides [31]. The glycosylation was performed on solid-phase using trichloroacetimidate donors, with the aglycone attached to the resin by a new selenium-based safety-catch linker [32]. The monosaccharide

analog proved to be less active than the parent vancomycin against all bacterial strains. Having established the importance of the vancosamine moiety for antibacterial activity Nicolaou and co-workers turned their attention to the modification of the existing glycan by reductive amination. Reaction of vancomycin with a variety of substituted benzaldehydes (containing terminal alkenes or thioacetates) yielded a library of vancomycin analogs (Figure 5a). Biological evaluation of this library revealed several highly potent compounds effective against vancomycin-resistant strains. Dimerization of these compounds by disulfide formation and olefin metathesis led to the identification of an additional set of highly potent antibiotics [33**]. In this case, the discovery of active compounds was facilitated through the use of target-accelerated combinatorial synthesis (or dynamic combinatorial synthesis) [34,35].

It has been suggested that glycolipid derivatives of vancomycin (i.e. compounds containing a lipid-functionalized disaccharide) are active against resistant strains of bacteria because of their ability to inhibit the transglycosylation step of peptidoglycan biosynthesis [36,37]. If this model is correct, it should be possible to improve the activity of vancomycin derivatives by optimizing the glycolipid moiety for inhibition of transglycosylation. In order to test this hypothesis, Kahne and co-workers [38] devised a strategy for the synthesis of a new class of vancomycin analogs, termed hybrid glycopeptide antibiotics. To illustrate their approach, the aglycone was modified by alkylation with a synthetic disaccharide, corresponding to an analog of the known transglycosylase inhibitor moenomycin (Figure 5b). This disaccharide had been identified from a combinatorial library of moenomycin analogs [39]. The resulting hybrid

Figure 5



Strategies for the synthesis of vancomycin analogs. (a) Nicolaou's synthesis of vancomycin analogs by reductive amination with benzaldehyde derivatives, containing terminal alkenes and thioacetates [31]. Dimerization of the vancomycin analogs (by disulfide formation or

olefin metathesis) led to the identification of potent antibiotics with activity against resistant bacterial strains [33**]. (b) Kahne's hybrid glycopeptide antibiotic, containing a disaccharide analog of the transglycosylase inhibitor moenomycin [38].

molecule, which contains the vancomycin aglycone in place of the lipid moiety, exhibits antibiotic activity far exceeding that of the individual components. This approach should greatly facilitate the synthesis of a large collection of vancomycin analogs, because the synthetically challenging glycosidic linkage is replaced with a simple ethylene glycol linker.

Conclusions

In light of the biological importance of oligosaccharides [40], the development of new strategies for their preparation is key to the advancement of our understanding of various carbohydrate-protein interactions and the discovery of new therapeutic agents. The application of combinatorial synthesis to the production of carbohydrate-based libraries has received increased attention in recent years. Combinatorial strategies have been applied to the discovery of new carbohydrate-based antibiotics, including derivatives of vancomycin [31,33,38] and aminoglycosides [29], and novel one-pot glycosylation strategies have been employed for the generation of oligosaccharide libraries [6,7]. Recent advances in solid-phase oligosaccharide synthesis, resulting in the development of an automated synthesizer [15], are expected to facilitate future progress in the assembly of carbohydrate-based libraries.

Acknowledgements

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Carbohydrate diversity: synthesis of glycoconjugates and complex carbohydrates

Alexandra Hölemann and Peter H Seeberger*

The fundamental role of glycoconjugates in many biological processes is now well appreciated and has intensified the development of innovative and improved synthetic strategies. All areas of synthetic methodology have seen major advances and many complex, highly branched carbohydrates and glycoproteins have been prepared using solution- and/or solid-phase approaches. The development of an automated oligosaccharide synthesizer provides rapid access to biologically relevant compounds. These chemical approaches help to produce sufficient quantities of defined oligosaccharides for biological studies. Synthetic chemistry also supports an improved understanding of glycobiology and will eventually result in the discovery of new therapeutics.

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Abbreviations

GlcNAc *N*-acetylglucosamine
GPI glycosylphosphatidylinositol
HIV human immunodeficiency virus
PSA prostate-specific antigen

Introduction

In addition to oligopeptides and oligonucleotides, oligosaccharides (glycans) constitute the third major class of naturally occurring biopolymers that play a fundamental role in many important biological processes. Glycans are commonly found in nature as glycoconjugates (glycoproteins or glycolipids) that show high structural diversity, greatly exceeding the diversity of proteins and nucleic acids.

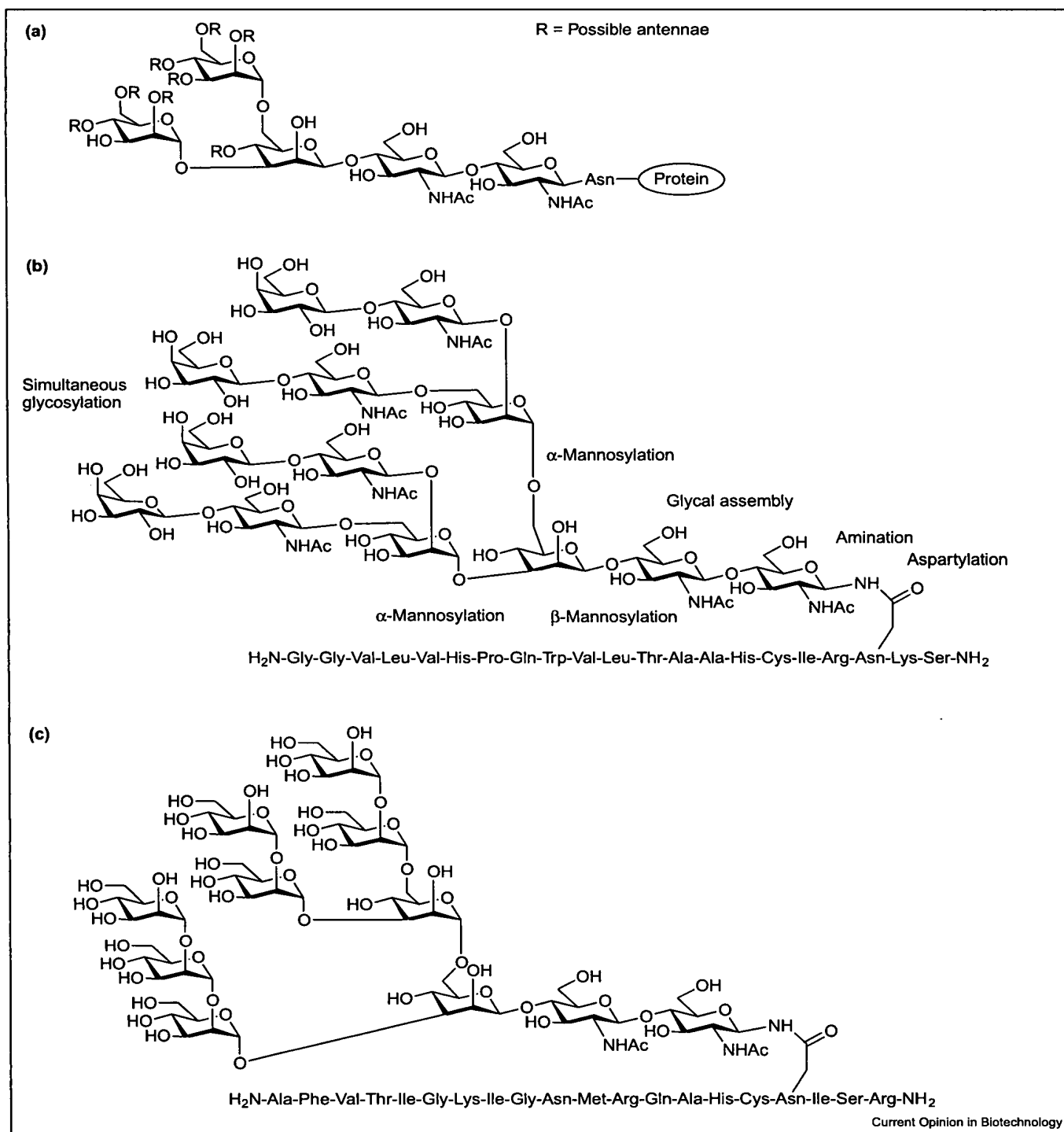
In contrast to linear oligopeptides and oligonucleotides, oligosaccharides are often complex branched molecules and the glycan core is commonly attached to proteins and

lipids. In nature, three major classes of glycans exist: *N*-linked glycans, *O*-linked glycans and glycosylphosphatidylinositol (GPI) anchors. Intensive research into the biological role of carbohydrates has led to an increased need for sufficient quantities of natural and modified glycoproteins; however, the isolation of carbohydrates from natural sources is extremely difficult owing to their structural complexity. Access to pure carbohydrates for biological, biochemical, biophysical and medicinal studies therefore relies on chemical and enzymatic synthesis [1,2]. Remarkable progress has been made in this area; however, further innovations are required to handle the structural complexity of oligosaccharides. Their preparation is technically difficult, extremely time-consuming and performed by a few specialized laboratories. The introduction of solid-phase synthesis strategies has significantly improved carbohydrate assembly, as an excess of reagent can be used to ensure high yields and to reduce the number of purification steps. The development of an automated oligosaccharide synthesizer [3*,4*,5**] has led to rapid access to complex carbohydrates of biological relevance. This review highlights recent advances in the synthesis of complex oligosaccharides and glycoproteins, primarily focusing on strategies published in the past two years.

N-Linked glycoproteins

N-Linked glycoproteins (*N*-glycans) are the most abundant in nature and are commonly divided into four groups: high-mannose, complex, hybrid and poly-*N*-acetylglucosamine glycans. Although the structural details are well established, little is known about their structure–activity relationship. In *N*-glycans, the oligosaccharide sidechain is attached to the protein via an asparagine amino acid. All *N*-glycans share the common pentasaccharide core structure (mannose)₃(*N*-acetylglucosamine)₂ (Man₃GlcNAc₂) shown in Figure 1a. Structural diversity is generated by variation in the substitution pattern of the pentasaccharide core, in the degree of branching and in the terminal sugars. The pentasaccharide core can be extended by up to five antennae. The preparation of the basic structure contains several synthetic challenges, including branching and the inclusion of a β -mannoside. Recently, two efficient partial syntheses of the core structure have been accomplished [6,7], selectively establishing the β -mannosidic linkage. The orthogonally protected β -mannosylated chitobiose trisaccharide with a terminal azido group serves as a key building block in the preparation of complex *N*-glycans. The entire pentasaccharide has been synthesized recently by Danishefsky and colleagues [8]

Figure 1



N-Linked glycoproteins. (a) Structure of the core pentasaccharide common to all *N*-glycans. The core structure can be extended by up to five antennae (R). (b) Structure of a prostate-specific antigen (PSA) glycopeptide. The crucial retrosynthetic steps of Danishefsky's [21*] strategy are shown. (c) Structure of the gp120 glycopeptide fragment, which is a possible target for an anti-HIV-vaccine. Protein sequences are shown using the three-letter amino acid code.

using Crich's β -mannosylation methodology [6] followed by a simultaneous di- α -mannosylation with a thiomannoside donor.

As an alternative to these solution-phase preparations, the synthesis of the core pentasaccharide selectively functionalized with one *N*-acetylglucosamine residue has been performed recently using a solid-phase approach [9]. The first automated solid-phase oligosaccharide synthesizer [5**] has been used to efficiently prepare the core pentasaccharide [10] by using an octenediol functionalized Merrifield's resin and three different building blocks: two monosaccharides and one disaccharide already containing the β -mannosidic linkage. Branching was achieved by simultaneous dimannosylation of the trisaccharide core.

Innovative synthetic methods have also provided access to more complex and highly branched *N*-glycans. Weiss and Unverzagt [11] have developed a general strategy for the preparation of multiantennary *N*-glycans. Crucial challenges in the synthesis of these sterically crowded bi- to tetra-antennary compounds is the sequence of introducing the building blocks and the steric demand of the building blocks. Complex biantennary *N*-glycans are also accessible via chemoenzymatic total synthesis. Elongation of synthetic oligosaccharides has been performed using glycosyltransferases to give full-length *N*-glycans [12,13].

Synthetic oligosaccharides are useful in gaining a more detailed understanding of glycoprotein quality control. In particular, maintenance of the integrity of protein folding has recently received significant attention. Ito and colleagues [14,15] accomplished a convergent and stereoselective route to the nonasaccharide $\text{Man}_8\text{GlcNAc}_2$ and the monoglucosylated dodecasaccharide $\alpha\text{-Glc}_1\text{Man}_9\text{GlcNAc}_2$, a putative ligand of the molecular chaperones calnexin and calreticulin. These synthetic oligosaccharides might serve as molecular probes to detect glycoprotein-mannosidase-like protein recognition.

Glycoproteins are also important in the context of diagnostics, therapeutics and vaccines. The integration of oligosaccharides into glycoproteins is realized by converting them into anomeric glycosylamines, which is either performed by treatment with ammonium hydrogencarbonate or by reduction of anomeric glycosyl azides, and subsequent attachment to the peptide chain [16–18]. Guo and colleagues [19] attached a fucosylated trisaccharide to the peptide of the CD52 antigen by using a solution-phase synthesis with solid-phase workup or a combined solution- and solid-phase approach. More complex oligosaccharides containing two thiol residues were linked to the same peptide by 9-fluorenylmethoxycarbonyl (Fmoc)-based solid-phase peptide synthesis [20]. Because of their short peptide chain containing only 12

amino acids, their simple glycosylation pattern and their interesting bioactivity, these glycopeptides serve as useful models to study structure–activity relationships. The development of a universal strategy [21*] for the preparation of complex multibranched *N*-acetylglucosamine-type glycans from common precursors has led to the first chemical synthesis of normal and transformed prostate-specific antigen (PSA) glycopeptides (Figure 1b). PSA has been identified as a highly specific cancer marker that might enable the early diagnosis of prostate tumours.

N-Linked carbohydrates also play an important role in human immunodeficiency virus (HIV) retroviral pathogenesis. The HIV-1 surface envelope glycoprotein gp120 is highly glycosylated containing up to 24 *N*-linked high-mannose carbohydrates and shows biological functions in helper T-lymphocyte infections [22]. Seeberger and colleagues [23] developed a linear solution-phase synthesis of a triantennary high-mannose nonasaccharide from gp120 using just three monosaccharide building blocks. Employing a reactivity-based one-pot self-condensation approach, Wong and coworkers [24] prepared several high-mannose oligosaccharides, which efficiently inhibit the binding of the antibody 2G12 to gp120. More recently, Danishefsky and colleagues [25**,26**] described the first chemical synthesis of HIV gp120 fragments (Figure 1c), which serve as targets for an anti-HIV vaccine.

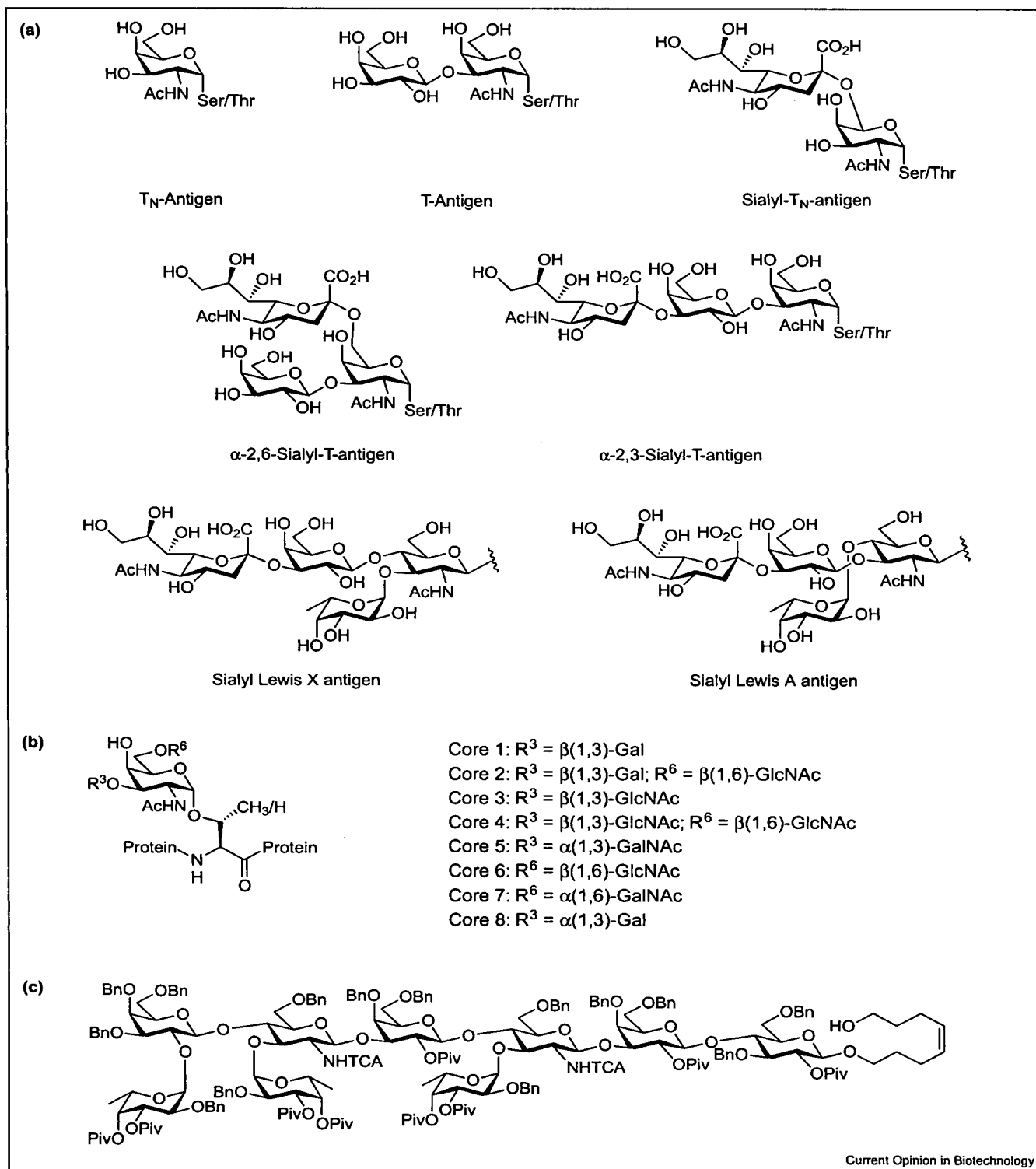
Many important glycoproteins are multiply glycosylated at fixed sites. Danishefsky's laboratory [27] recently disclosed a convergent method for the preparation of bifunctional glycopeptides: two glycopeptides are synthesized separately from their glycan and peptide precursors using standard procedures and subsequently coupled to yield the bifunctional compounds.

O-Linked glycoproteins

A second major group of biologically important glycoproteins are *O*-linked glycoproteins (*O*-glycans). The carbohydrate residue in *O*-glycans is covalently attached to the peptide backbone via the hydroxyl group of serine, threonine, tyrosine, hydroxyproline, hydroxylysine or another hydroxylated amino acid. In contrast to *N*-glycans, these glycoproteins show a higher degree of structural diversity and do not share a common core structure. Additional variety arises from further carbohydrate elongations of these backbones.

Tumour-associated antigens (Figure 2a) like the T_N -, T -, sialyl- T_N and sialyl- T antigens as well as the sialyl Lewis X and sialyl Lewis A antigens were first found in mucins. Mucins are a class of highly *O*-glycosylated proteins present on the surface of various types of epithelial cells. In normal tissue, the peptide backbone carries several complex oligosaccharides derived from the glycan core structures shown in Figure 2b, which are characterized by

Figure 2



O-Linked glycoproteins. (a) Structures of tumour-associated carbohydrate antigens that were first discovered in mucins. (b) Core structures of mucin-type O-linked glycans, a class of highly O-glycosylated proteins. (c) Structure of the Le^y-Le^x tumour marker. Ac, acetyl; Bn, benzyl; Piv, pivaloyl; TCA, trichloroacetyl.

an *N*-acetylgalactosamine unit α -*O*-linked to serine or threonine. An increased expression of mucins is usually prevalent in tumour cells, where the carbohydrate chains are modified due to incomplete glycosylation and premature sialylation. As tumour-associated glycans with peptide sequences of mucins constitute a promising target for the development of synthetic antitumour vaccines, the chemical synthesis of such glycoconjugates has received considerable attention and several reviews devoted to this field of research have been published [28–30,31*].

A solid-phase approach [32,33] has been used for the stereoselective construction of several different mucin-type *O*-glycans. Stepwise elongation of the carbohydrate led to the required highly glycosylated amino acid building blocks, which were then incorporated into a solid-phase glycopeptide synthesis. Other branched *O*-glycans have recently been prepared by an efficient one-pot glycosylation approach using either glycosyl fluoride [34] or thioglycoside [35] building blocks. As sialylated derivatives of tumour-associated antigens are also present on the surface of cancer cells, the preparation of *O*-linked sialyl oligosaccharides is important. Paulson and colleagues [36] demonstrated that recombinant sialyltransferases are ideal catalysts for the simple and efficient preparation of *O*-linked sialyl oligosaccharides by elongation of a synthetic glycosyl amino acid.

The application of non-natural amino acids in carbohydrate vaccines has also attracted considerable attention [37], as these unnatural linkages might give an increased immune response. Danishefsky's group [38] investigated the synthesis of different glycosyl hydroxynorleucines, each containing a tumour-associated carbohydrate antigen. While the glycosylation of trichloroacetimidate donors with the amino acid predominately afforded the corresponding α -*O*-linked product, the reaction with a glycol epoxide donor provided the β -*O*-linked product. The glycol methodology was also successfully applied to the synthesis of Lewis Y- and Globo-H-containing amino acids.

More recently, an automated synthesizer has been used to accelerate the synthesis of the Lewis^y-Lewis^x tumour marker (Figure 2c) and the Lewis X and Lewis Y blood group antigens [39**]. Only five monomers were necessary for the efficient construction of the three target structures.

GPI anchors

GPI-anchored proteins are involved in many biological and physiological processes and have attracted considerable attention since the first structure determination of a GPI in 1988 [40]. These naturally occurring glycolipids serve to attach proteins or glycoproteins onto eukaryotic cell membranes. All reported GPI structures share the

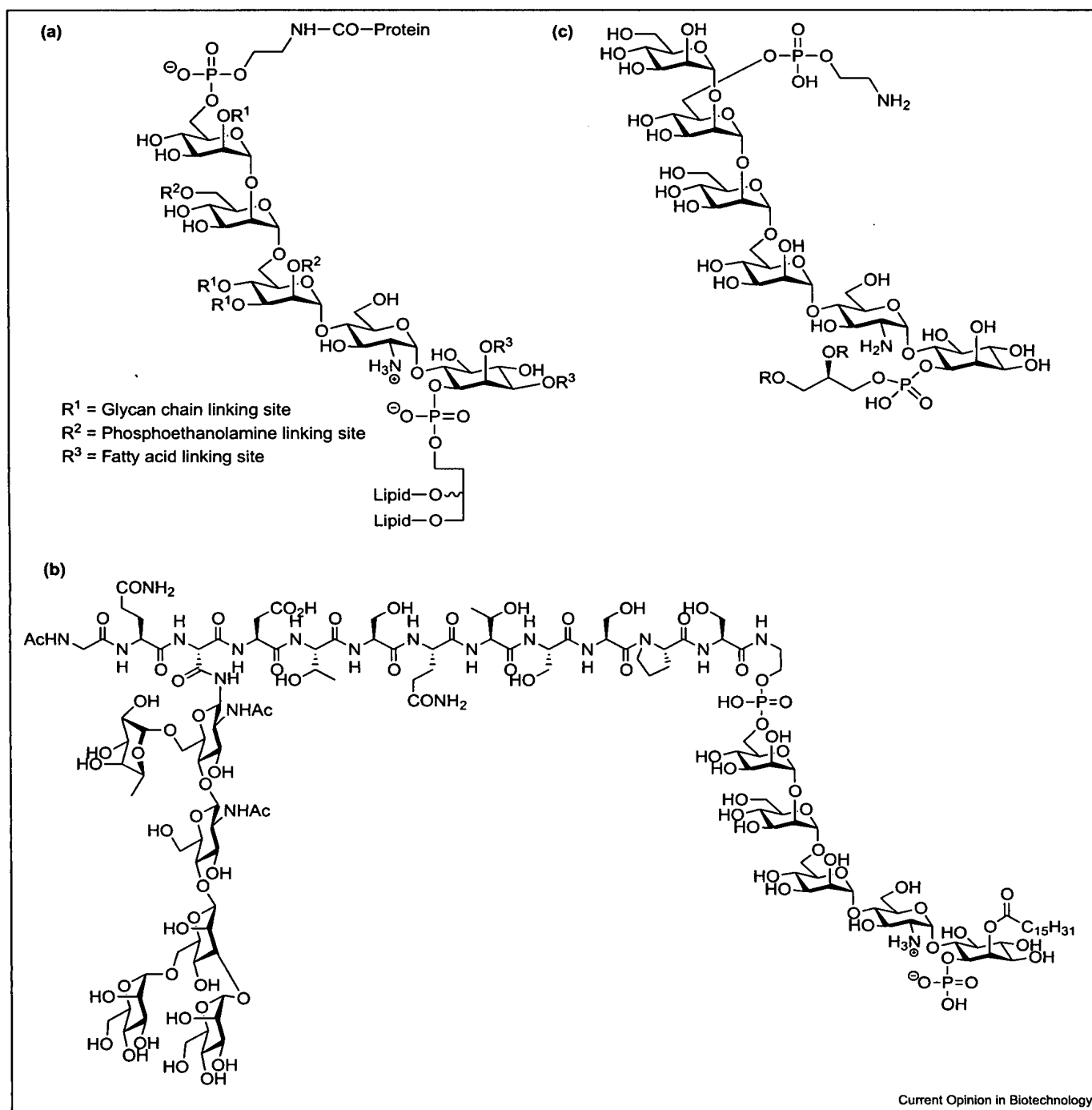
basic core structure shown in Figure 3a with a linear tetrasaccharide attached to the 6-*O*-position of inositol. Besides this conserved general structure, considerable diversity exists within the GPI anchor family based on the variation of the substitution pattern on this pseudo-pentasaccharide backbone. In most cases, the core is further modified by species-specific carbohydrates, additional phosphoethanolamine units and variations in the lipid moiety. Proteins or glycoproteins are linked to the non-reducing end by their C termini or a phosphoethanolamine group. Owing to the structural complexity of the GPI anchors that requires a detailed knowledge of lipid, phosphate and oligosaccharide chemistry, many chemists have focused on the synthesis of these motifs [41*].

A linear solution-phase approach allows for the construction of complex GPI anchors and for the preparation of an orthogonally protected derivative of the phosphorylated pseudo-pentasaccharide core [42]. Another variable concept for the preparation of branched GPIs was developed by Pekari and Schmidt [43]. The efficiency of this approach was demonstrated by the synthesis of the GPI anchors of rat brain Thy-1 and scrapie prion protein in their water-soluble and lipidated forms. This approach also allows further attachment of peptide residues or biological markers to the GPI anchor. Reichardt and Martin-Lomas [44] reported a soluble support-based approach for the synthesis of the GPI backbone. This method, using a polyethylene glycol-grafted polystyrene resin functionalized with a Wang-chloride linker, can be applied to the preparation of a small library of GPI precursors.

CD52 antigens, simple GPI-anchored glycopeptides, are present on eukaryotic cells and play an important role in the human immune system. Initial studies aimed at the synthesis of sperm CD52, including the preparation of an acylated inositol [45] and the linkage to the peptide [46], were performed by Guo and colleagues. More recently, they reported [47**] the first synthesis of a skeleton structure of sperm CD52. In their strategy the glycopeptide and the GPI anchor were prepared separately and subsequently linked by an amide bond to give the glycopeptide–GPI conjugate (Figure 3b).

Synthetic GPIs are promising vaccine candidates against malaria, as shown in a mouse model [48]. Annually, malaria infects 5–10% of the world's population and kills about 3 million people each year. The malaria parasite *Plasmodium falciparum* expresses a large amount of GPI anchored to a protein, and the GPI structure (Figure 3c) has been identified as the malaria toxin. A solution-phase synthesis of two malaria vaccine candidates with a pseudo-hexasaccharide backbone has recently been reported by Seeberger and colleagues [49]. This strategy allows for scale-up to procure compounds for preclinical

Figure 3



GPI anchors. (a) Basic core structure of all GPI anchors. (b) Skeleton structure of sperm CD52. (c) Structure of the malaria GPI vaccine candidate.

and clinical trials. The authors also demonstrated that the synthesis of this target can be automated effectively [50**]. The fully protected oligosaccharide was obtained

in only 9 h starting from four monosaccharides and one disaccharide building block. Fraser-Reid and coworkers [51,52**] developed a method for the solution-phase

synthesis of a fully lipidated and phosphorylated malarial GPI pseudo-pentasaccharide using orthoesters and methyl α -D-glucopyranoside as the key building blocks.

Conclusions

Innovative synthetic methods are an important tool to create diverse carbohydrates. Recent advances in the preparation of complex oligosaccharides as well as entire glycoproteins containing *N*-glycans, *O*-glycans and GPI anchors have been highlighted in this review. Highly branched carbohydrates and biologically relevant oligosaccharides are now accessible via these methods, providing sufficient quantities for biological studies. The availability of defined synthetic glycoproteins and glycolipids will significantly support biological investigations. The development of new strategies for the preparation of carbohydrates is fundamental for the understanding of carbohydrate–protein interactions, biosynthetic pathways and structure–activity relationships and will allow for the discovery of new targets for therapeutics, diagnostics and vaccines. The introduction of an automated oligosaccharide synthesizer has greatly accelerated access to many highly branched carbohydrates, and a series of biologically relevant oligosaccharides has been efficiently prepared on this machine. Further improvement and extension of this technology could allow for the automated synthesis of complex glycoproteins, proteoglycans and glycolipids using only one instrument and will eventually enable even non-specialists to create biologically important compounds for biochemical, biophysical and medicinal applications.

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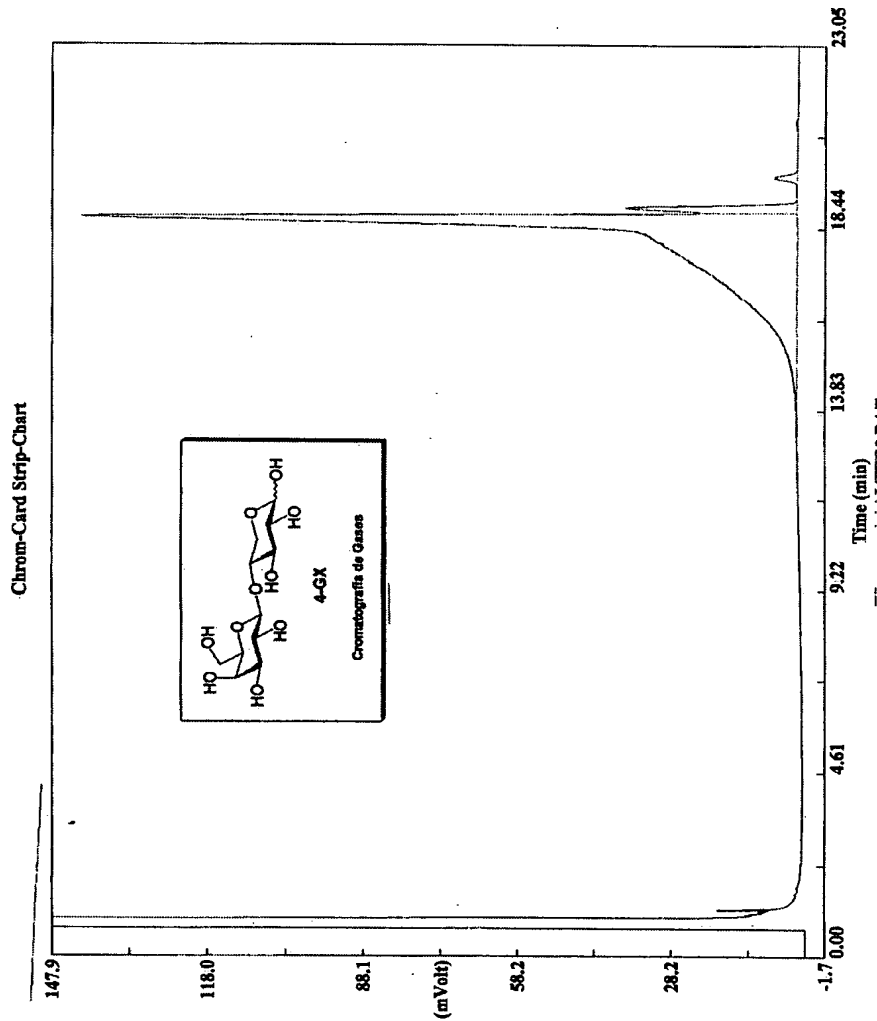
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Exhibit D

Gas chromatogram of 4-galactosyl-xylose



Retention Time (min)	Peak Height (uV)	Area (.1*uV*sec)	Area % (%)	Plates (N)
18.700	138499	46240450	92.566	36622
18.928	33256	3268899	6.540	123711
19.713	4427	406455	0.814	104794
21.075	362	40018	0.080	81899
	192093	49953820		

ear region of the adsorption isotherm, the retention time and the peak width, defined as the first absolute moment μ_1 and the second central moment μ_2 , respectively, are functions of the quantities that characterize the chemical nature and texture of a solid packing [371-375]:

$$\mu_1 = f_1(K_s) \quad (175)$$

$$\mu_2 = f_2(K_s, k_a, e', D_{\text{int}}^{-1}) \quad (176)$$

where

K_s = partition coefficient in GSC,

k_a = adsorption coefficient,

e' = internal porosity of the particles with respect to the pore space (which, contrary to e_0 , the interparticle porosity, was not considered in eqns. (55) and (56),

D_{int} = effective diffusion coefficient of the separated substances in the pores of the solid.

Owing to the proportionality between K_s and the specific retention volume in GSC, V_s [eqn. (20)], the retention increases with increasing adsorption equilibrium constant, which in turn depends on the strength of the interaction of the compound to be adsorbed/desorbed with the solid phase. The differences in the K_s values for solutes with different chemical structures will be large, hence accomplishing the separation ($\mu_1 = f_1(K_s)$).

Strong adsorption invariably broadens the peak, as is apparent from eqn. (176) where K_s is involved, and as is confirmed by experience, i.e., it affects the efficiency and separability. A principal means of improving the peak width consists in the selection of adsorbents with a favourable pore size distribution, as μ_2 [eqn. (176)] depends on e' and on the reciprocal of the diffusion coefficient D_{int} in the pores of the solid. In narrow pores, e.g., with pore diameters 10 nm, the Knudsen diffusion is predominant, i.e., collisions of sample molecules with the pore walls take place more often than with other sample molecules or with molecules of the carrier gas. This special diffusion, the rate of which increases linearly with increasing pore diameter, is very slow (e.g., for n-hexane at 10 Torr, $D_{\text{kn}} = 0.0202 \text{ cm}^2/\text{s}$, compared with the bulk diffusion coefficient for a hydrogen-n-hexane mixture of $D = 0.5148 \text{ cm}^2/\text{s}$ [375, 376]). In wide pores, i.e., with pore diameters > 200 nm, the rate of diffusion is independent of the pore diameter and the effective diffusion coefficient is proportional to the bulk diffusion coefficient.

To summarize, there are two essential characteristics of adsorbents by which they can be classified: their chemical structure and their geometrical structure.

5.1.1. Classification According to Chemical Structure

Based on the chemical nature of the adsorbent surface, different kinds of interactions with different sample molecules can occur. *Kiselev*, whose proposed classification [377, 378-379] has been generally accepted and applied, subdivides adsorbents into three groups (I-III) and adsorbates into four groups (A-D).

Adsorbents of type I

Non-specific adsorbents, which do not have any functional groups or ions on the surface and hence are not capable of specifically interacting with adsorbates. The interaction with all types of sample molecules A-D proceeds non-specifically. Adsorbents of this type are saturated hydrocarbons (in crystalline or solid polymer modification or as a layer on a suitable supporting adsorbent), graphite or rare gas crystals. The most important adsorbent of this type is graphitized thermal carbon black (GTCB) which in its adsorption properties approaches an ideally non-specific adsorbent when prepared or pre-treated in a suitable manner.

The adsorbed molecules are arranged in such way that they contact the highest possible number of surface atoms.

Owing to their structure, which is similar to that of graphite, the inorganic adsorbents boron nitride (BN), and sulphides of some metals (e.g., MoS_2) can be included in this group [379, 380].

Adsorbents of type II

Specific adsorbents exhibiting positive partial charges localized on the surface. In addition to the dispersion interactions that occur on any adsorbent independent of its type, specific interactions develop, resulting in an orientation and localization of the adsorbate molecules at the sites with the highest charge. Especially salts, in which the positive charge is concentrated on cations of small radius whereas the negative charge is distributed over a relatively large volume, belong to this type (e.g., BaSO_4). Zeolites, the cations of which have small atomic volumes, whereas the negative charge is distributed over the inner bonds of a large complex anion formed from AlO_4^- and SiO_4 tetrahedra, are also of this type [379].

However, the most significant representatives of this type are adsorbents with functional groups of protonated acids, such as hydroxylated silica gels, and with aprotic Lewis centres on the surface.

Sample molecules of type A (saturated hydrocarbons, rare gases) are adsorbed non-specifically, as only dispersion forces can become effective. Molecules of type B, C and D can be adsorbed specifically.

Type B include molecules with an electron density localized on some bonds or atoms: π -bonds (unsaturated and aromatic hydrocarbons); functional groups, the atoms of which exhibit unshared electron pairs (ethers, ketones, tertiary amines, pyridine, nitriles); high quadrupole moments (N_2 molecules)

The interaction between type B adsorbates and type II adsorbents occurs between the centres of higher electron density (sample molecule) and the positive charge of the adsorbent (for example, the acidic proton of hydroxylated silica gel or an appropriate cation (Li, Na, Mg, Ca) in zeolites or aprotic Lewis centre (Al, B) on the surface).

Type C molecules have a localized positive charge on a metal atom and the excess of the electron density is distributed over adjacent bonds (organometallic compounds). Because of the high reactivity of many organometallic compounds and of the risk of chemisorption, there have been only a few investigations of this interaction.

Type D molecules contain peripheral functional groups (OH, NH, etc.), the electron density of which is increased on one of the atoms (O, N) and diminished on the other (H). This group includes water, alcohols and primary and secondary amines. The specific interactions of type D adsorbates with type II adsorbents mainly involve forces between the positive charge centres of the adsorbent and the lone electron pairs of the O or N atoms of the sample molecules.

Adsorbents of type III

Specific adsorbents bearing centres of higher electron density on the surface. To this group belong polymers such as polyacrylonitrile, copolymers of vinylpyridine and divinylbenzene and polymers with $\text{C}=\text{O}$ and $-\text{O}-$ groups on the surface. Porous polymers based on styrene-ethylvinylbenzene, cross-linked with divinylbenzene, varied by applying different polymerization initiators with various functional groups, may also be included in this group, even if non-specific dispersion forces preponderate. Type III adsorbents include also crystal surfaces formed by anions, and especially chemically modified adsorbents or non-specific adsorbents covered by a dense monolayer of suitable substances, hence creating negative charge centres on the surface.

Adsorbents of type III interact non-specifically with adsorbates of type A and specifically

with types such as B, C and D by forces between the negative charge on the adsorbent's surface and the positive charge of the metal atom (C) or of the functional group's (OH, NH) proton (D) or of the dipole or an induced dipole (B).

5.1.2. Classification According to Geometrical Structure

We had stated that the geometry of the adsorbents influences especially the capacity term in eqn. (100). Hence the surface area should be as high as possible in order to increase this term. However, there are serious reservations. Increasing the surface area means either increasing the dispersity (with the consequence of an increase in heterogeneity due to the increasing contact points between the particles) or narrowing the pore diameters (with the disadvantage of Knudsen diffusion). The outcome of numerous investigations in this field, among which especially the work of *Kiselev* should be given prominence, has been that difficulties of this kind, having retarded the development of GSC for a long time, have been surmounted [379].

The role of the surface area can be derived from basic equations in Chapter 2. For infinitely small (zero) samples, the net retention volume V_N , under equilibrium conditions, is equal to the Henry constant of the adsorption equilibrium [379]:

$$V_N = K_H = \lim_{n_{ads} \rightarrow 0} \left(\frac{n_{ads}}{c} \right) \quad (177)$$

where c is the concentration of the sample in the gas phase. If we consider the total surface area of the adsorbent in the column, $m_A S_A$, where m_A = weight of the adsorbent and S_A = specific surface area of the adsorbent, we obtain (from eqns. (11) and (20)), neglecting the temperature,

$$V_s = \frac{V_N}{m_A S_A} = K_s,$$

which is the adsorption coefficient (or the Henry constant referred to unit surface area of the adsorbent).

From $V_N = K_H$ we obtain the correlation of both constants K_H and K_s with the geometrical parameter:

$$V_N = K_H = m_A S_A V_s = m_A S_A K_s. \quad (178)$$

Hence V_N , the net retention volume, can be influenced by both the column parameters (weight of the adsorbent m_A) and the geometrical characteristic of the adsorbent, its specific surface area S_A . K_s , however, can be influenced by the chemical nature and structure of both the interacting adsorbent and adsorbate, expressed by analogy with eqn. (189a) as the partial molar adsorption enthalpy [381]:

$$\frac{d \ln K_s}{dT} = \frac{\Delta H_A}{RT^2}. \quad (179)$$

As ΔH_A , the partial molar adsorption enthalpy, changes only slightly with the temperature, we can write [379]

$$\ln K_s \approx -\frac{\Delta H_A}{RT} + \frac{\Delta S_A}{R} + 1 \quad (180)$$

or

$$K_s \approx \exp \left[\frac{\Delta S_A}{R} + 1 \right] \exp \left[\frac{-\Delta H_A}{RT} \right], \quad (180a)$$

where ΔS_A = partial molar adsorption entropy of the adsorbate for the transition from the standard state of the gas volume with concentration c^0 into the standard adsorbate state with an adsorption concentration Γ^0 .

Eqn. (180a) shows the exponential dependence of K_s on temperature, the third essential parameter in GSC, in addition to the adsorbent's chemical structure and geometrical structure. Eqns. (178) and (180a) demonstrate that even adsorbents with small specific surfaces areas permit the separation of weakly adsorbable gases, provided that the column temperature is decreased accordingly, hence increasing K_s and thus also its product with the surface area, $m_A S_A K_s$ [379]. The alternative, or better for completion when separating low boiling gases, is the use of adsorbents with small particle diameters and/or fine pores, hence increasing S_A and $m_A S_A$.

Kiselev and Yashin [377] classified adsorbents geometrically as follows.

- | | |
|--------|--|
| Type 1 | Non-porous adsorbents
Crystalline products with a smooth surface (sodium chloride, graphitized thermal carbon black, BN, MoS ₂)
S_A values 0.1–12 m ² /g. |
| Type 2 | Uniformly porous adsorbents with wide pores
Silica gels with pore diameters between 10 and 200 nm (but each silica gel product with narrowly distributed pore diameters!) (Porasil, Spherasil) and phases bonded chemically on silica gel (Durapak, etc.) as also some wide-pore styrene-divinylbenzene polymers (pore diameters 20–400 nm). |
| Type 3 | Uniformly porous adsorbents with narrow pores
Molecular sieves (zeolites), carbon molecular sieves, porous glasses, porous polymers. Pore diameters 10 nm. |
| Type 4 | Irregularly porous adsorbents
Active charcoal, alumina. Owing to the geometrical (and chemical!) heterogeneity [the pore diameters range from 2–20 nm (transition pores) up to >200 nm (macropores)], such adsorbents are not appropriate for GSC (with the exception of their use as enrichment materials), even though they were widely applied in the early years of gas chromatography. |

This classification is based on the existence and size of the pores. Porous adsorbents differ from non-porous solids by a void structure shaped from a system of pores. This structure can be characterized, independent of the chemical composition of the adsorbent, by the following quantities [382]:

- Specific surface area S_A (geometric size of the pore wall area per gram of adsorbent).
- Specific pore volume V_p (total pore volume per gram of adsorbent).
- Mean pore diameter d_{50} (average diameter of 50% of the pores; this value is identical with the maximum frequency only for a homogeneous pore size distribution).
- Pore size distribution (distribution function $d(V_p)/d(d_{50})$).

They can be determined by gas chromatography [381], mercury porosimetry and reversed size exclusion chromatography [383]. Important for porous adsorbents is the ratio of their pore diameters to the diameters of the adsorbate molecules. If this ratio is high, i.e., the pore diameters are much larger than the molecule diameters, then the adsorption equilibrium is established rapidly. If the pore diameters are similar in size to the adsorbate molecules, then the adsorption rate depends on both the pore shape and the size of the molecules. In narrow pores the adsorbed molecule may interact with surface atoms of the opposite pore walls, and the exchange of molecules with the mobile phase is delayed. Hence the adsorption behaviour

FRACTIONATION OF THE REACTION MIXTURE THROUGH A CARBON/CELITE COLUMN USING DIFFERENT SOLVENTS

In order to find the appropriate solvent system for the elution of the carbon/celite column, a typical reaction mixture was chromatographed using different water-alcohol mixtures as eluent. The results indicated that the volume of solvent was significantly reduced when a mixture of water:isopropanol was used as eluent.

Reaction conditions and results of fractionation:

a) Reaction (following the described procedure):

- Nitrophenyl galactopyranoside, 5g.
- Xylose, 25 g.
- β -galactosidase from *E. Coli*.
- Phosphate buffer (pH, 7.0), 330 mL.
- 37 °C.

b) Fractionation through carbon/celite column:

Once the reaction is finished, the crude mixture is fractionated through a carbon/celite column using mixtures of alcohols and water as the eluent. The results are summarized in the following Table.

Table

Eluent	Eluent gradient (ratio water:alcohol)	Total volume (litres) used
water:methanol	100:0 (initial) \rightarrow 70:30(final)	12.9
water:ethanol	100:0 (initial) \rightarrow 90:10 (final)	7.5
water:isopropanol	100:0 (initial) \rightarrow 92:8(final)	5.8
water:isopropanol	98:2 (initial) \rightarrow 95:5(final)	3.6